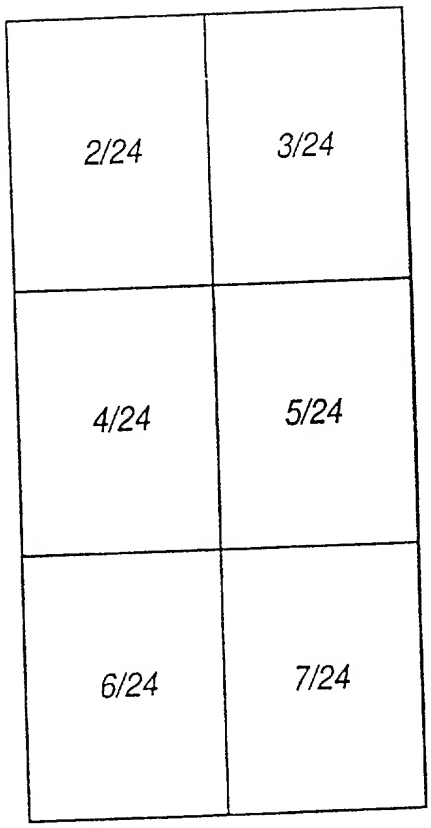


Fig. 1

```
-60   tgaaaagatagaataaatggcctcgtg

1     ATGGCGCGGCCAGCGCTGCTGGGCGAG
1      M  A  R  P  A  L  L  G  E

61    GGCCAAGTTGCCGCGGCCACAGAAGTT
21     G  Q  V  A  A  A  T  E  V

121   GAAAATCTCTGCACGATAATATGGACG
41     E  N  L  C  T  I  I  W  T

181   ACTCTCAGATATTTTAGTCACTTTGAT
61     T  L  R  Y  F  S  H  F  D

241   CATCGTAAAGAGGAATTACCCCTGGAT
81     H  R  K  E  E  L  P  L  D

301   AGTGCCAATGAAAGTGAGAAGCCTAGC
101    S  A  N  E  S  E  K  P  S

361   GGTGATCCTGAGTCCGCTGTGACTGAG
121    G  D  P  E  S  A  V  T  E

421   AAGTGTTCCTGGCTCCCTGGAAGGAAT
141    K  C  S  W  L  P  G  R  N
```

Fig. 1(i)

```
ccgaattcggcacgagccgaggcgagggcctgc

CTGTTGGTGCTGCTACTGTGGACCGCCACCGTG
 L  L  V  L  L  L  W  T  A  T  V

CAGCCACCTGTGACGAATTTGAGCGTCTCTGTC
 Q  P  P  V  T  N  L  S  V  S  V

TGGAGTCCTCCTGAAGGAGCCAGTCCAAATTGC
 W  S  P  P  E  G  A  S  P  N  C

GACCAACAGGATAAGAAAATTGCTCCAGAAACT
 D  Q  Q  D  K  K  I  A  P  E  T

GAGAAAATCTGTCTGCAGGTGGGCTCTCAGTGT
 E  K  I  C  L  Q  V  G  S  Q  C

CCTTTGGTGAAAAAGTGCATCTCACCCCCTGAA
 P  L  V  K  K  C  I  S  P  P  E

CTCAAGTGCATTTGGCATAACCTGAGCTATATG
 L  K  C  I  W  H  N  L  S  Y  M

ACAAGCCCTGACACACACTATACTCTGTACTAT
 T  S  P  D  T  H  Y  T  L  Y  Y
```

Fig. 1(ii)

```
481  TGGTACAGCAGCCTGGACAAAAGTCGT
161   W  Y  S  S  L  E  K  S  R

541  ATTGCTTGTTCCTTTAAATTGACTAAA
181   I  A  C  S  F  K  L  T  K

601  ATAATGGTCAAGGATAATGCTGGGAAA
201   I  M  V  K  D  N  A  G  K

661  TCCTATGTGAAACCTGATCCTCCACAT
221   S  Y  V  K  P  D  P  P  H

721  TTAGTGCAGTGGAAGAATCCACAAAAT
241   L  V  Q  W  K  N  P  Q  N

781  GTCAATAATACTCAAACCGACCGACAT
261   V  N  N  T  Q  T  D  R  H

841  AATTCCGAATCTGATAGAAACATGGAG
281   N  S  E  S  D  R  N  M  E

901  GCCGACGCTGTCTACACAGTCAGAGTA
301   A  D  A  V  Y  T  V  R  V

961  AACAAACTGTGGAGTGATTGGAGTGAA
321   N  K  L  W  S  D  W  S  E
```

Fig. 1(iii)

```
CAATGTGAAAACATCTATAGAGAAGGTCAACAC
 Q  C  E  N  I  Y  R  E  G  Q  H

GTGGAACCTAGTTTTGAACATCAGAACGTTCAA
 V  E  P  S  F  E  H  Q  N  V  Q

ATTAGGCCATCCTGCAAAATAGTGTCTTTAACT
 I  R  P  S  C  K  I  V  S  L  T

ATTAAACATCTTCTCCTCAAAAATGGTGCCTTA
 I  K  H  L  L  L  K  N  G  A  L

TTTAGAAGCAGATGCTTAACTTATGAAGTGGAG
 F  R  S  R  C  L  T  Y  E  V  E

AATATTTTAGAGGTTGAAGAGGACAAATGCCAG
 N  I  L  E  V  E  E  D  K  C  Q

GGTACAAGTTGTTTCCAACTCCCTGGTGTTCTT
 G  T  S  C  F  Q  L  P  G  V  L

AGAGTCAAAACAAACAAGTTATGCTTTGATGAC
 R  V  K  T  N  K  L  C  F  D  D

GCACAGAGTATAGGTAAGGAGCAAAACTCCACC
 A  Q  S  I  G  K  E  Q  N  S  T
```

Fig. 1(iv)

```
1021  TTCTACACCACCATGTTACTCACCATT
341     F   Y   T   T   M   L   L   T   I

1081  CTTTTTTACCTGAAAAGGCTTAAGATC
361     L   F   Y   L   K   R   L   K   I

1141  ATTTTTAAAGAAATGTTTGGAGACCAG
381     I   F   K   E   M   F   G   D   Q

1201  ATCTATGAGAAACAATCCAAAGAAGAA
401     I   Y   E   K   Q   S   K   E   E

1261  AAAGCAGCTCCTTGAtggggagaagtg
421     K A A P *

1321  gatttattgcattctccatttgttatc
1381  cttgaaaaacaggcagctcctaagagc
1441  ccaaacccaaaggagctccttccaaga
1501  ccctaaaagcagatgttttgccaaatc
1561  accatcaattcatctaatcaggaattg
```

Fig. 1(v)

```
CCAGTCTTTGTCGCAGTGGCAGTCATAATCCTC
 P  V  F  V  A  V  A  V  I  I  L

ATTATATTTCCTCCAATTCCTGATCCTGGCAAG
 I  I  F  P  P  I  P  D  P  G  K

AATGATGATACCCTGCACTGGAAGAAGTATGAC
 N  D  D  T  L  H  W  K  K  Y  D

ACGGATTCTGTAGTGCTGATAGAAAACCTGAAG
 T  D  S  V  V  L  I  E  N  L  K

atttctttcttgccttcaatgtgaccctgtgaa


tgggggacttgttaaatagaaactgaaactact
cacaggtcttgatgtgacttttgcattgaaaac
aaagcaagagttcttctcgttccttgttccaat
cccaaactagaggacaaagacaagggacaatg
tgatggcttcctaaggaatctctgcttgctctg
```

Fig. 1(vi)

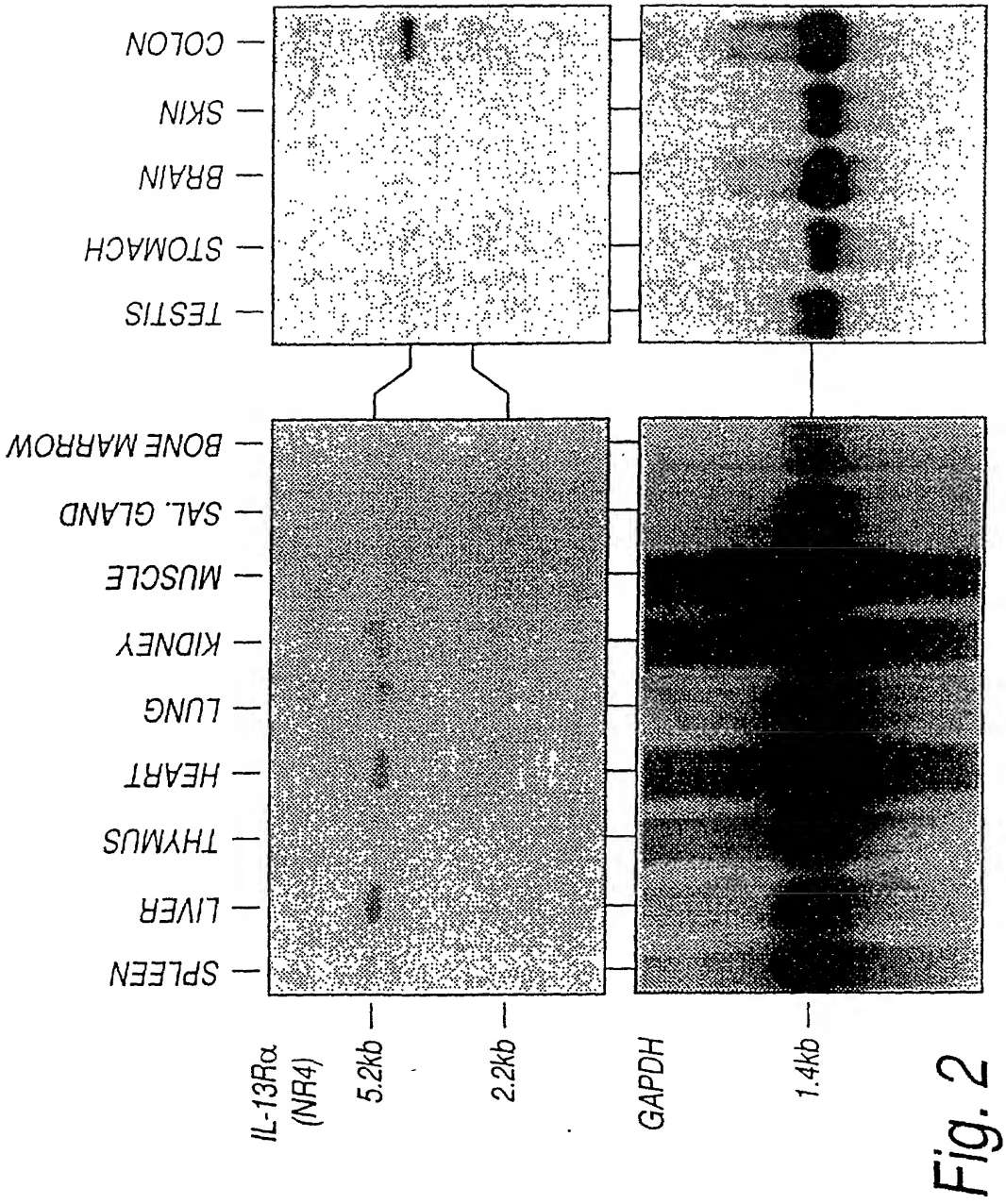

NR4 EXPRESSION IN MOUSE TISSUES
COLON
SKIN
BRAIN
STOMACH
TESTIS
BONE MARROW
SAL. GLAND
MUSCLE
KIDNEY
LUNG
HEART
THYMUS
LIVER
SPLEEN
IL-13Rα (NR4)
5.2kb
2.2kb
GAPDH
1.4kb

Fig. 2

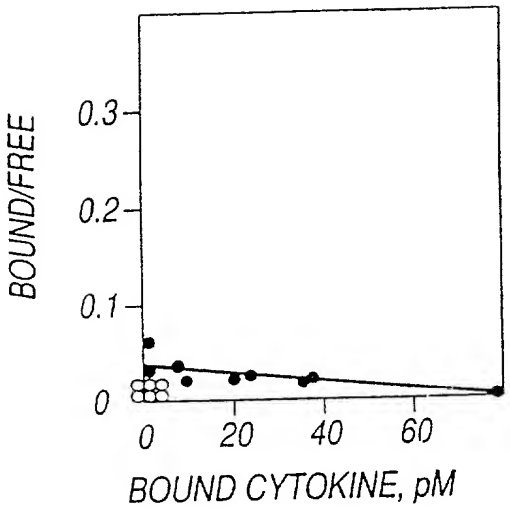


Fig. 3(A)

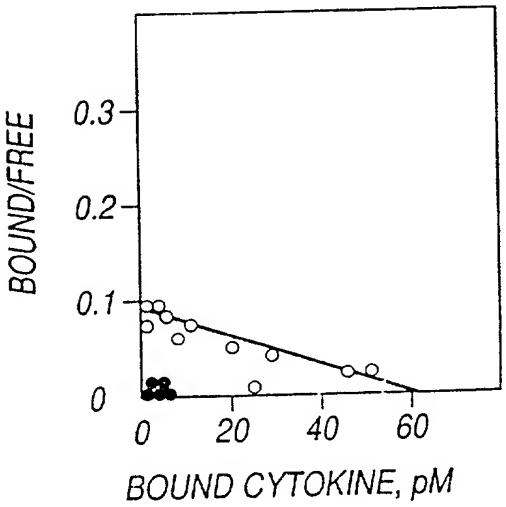


Fig. 3(B)

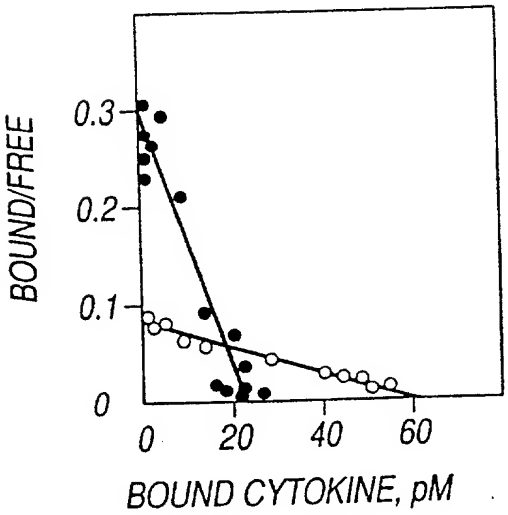


Fig. 3(C)

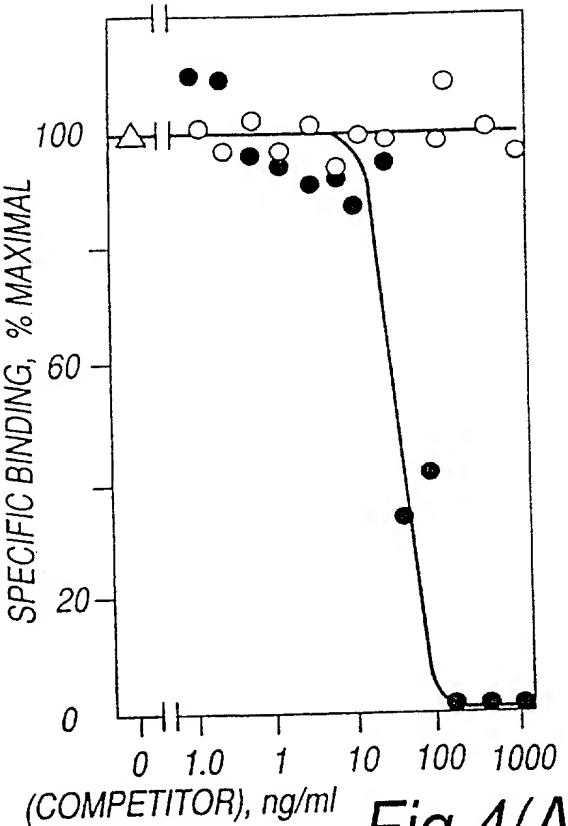

SPECIFIC BINDING, % MAXIMAL
100
60
20
0
0 1.0 1 10 100 1000
(COMPETITOR), ng/ml

Fig.4(A)

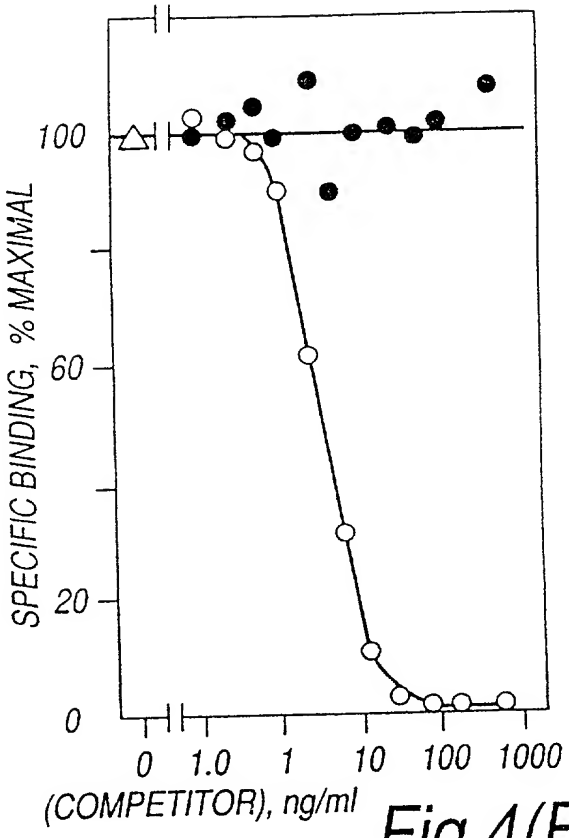
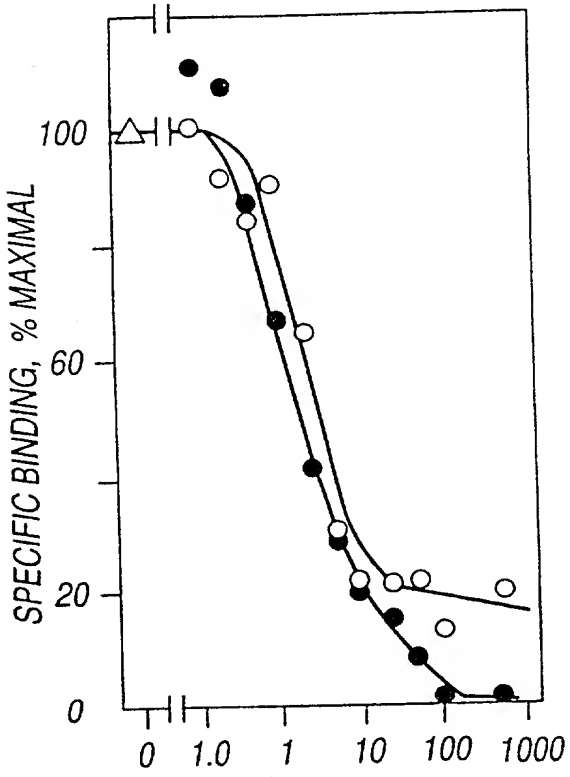
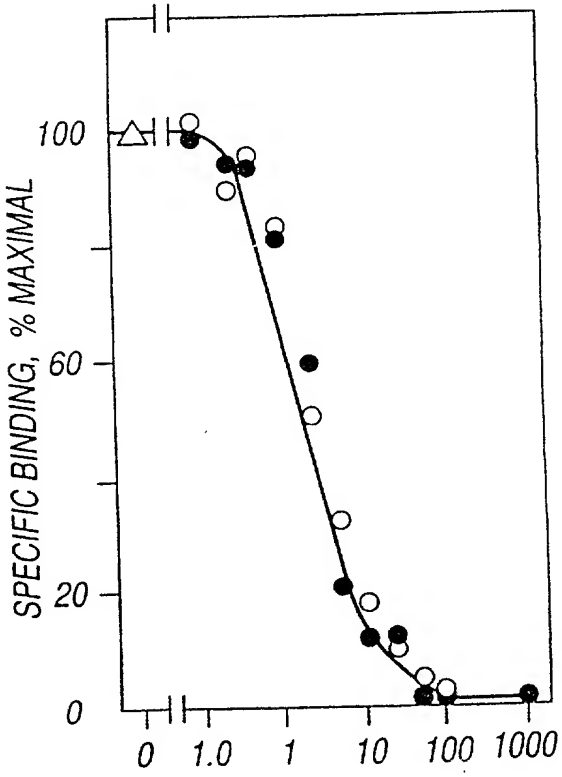

SPECIFIC BINDING, % MAXIMAL
100
60
20
0
0 1.0 1 10 100 1000
(COMPETITOR), ng/ml

Fig.4(B)


SPECIFIC BINDING, % MAXIMAL
100
60
20
0
0 1.0 1 10 100 1000


SPECIFIC BINDING, % MAXIMAL
100
60
20
0
0 1.0 1 10 100 1000

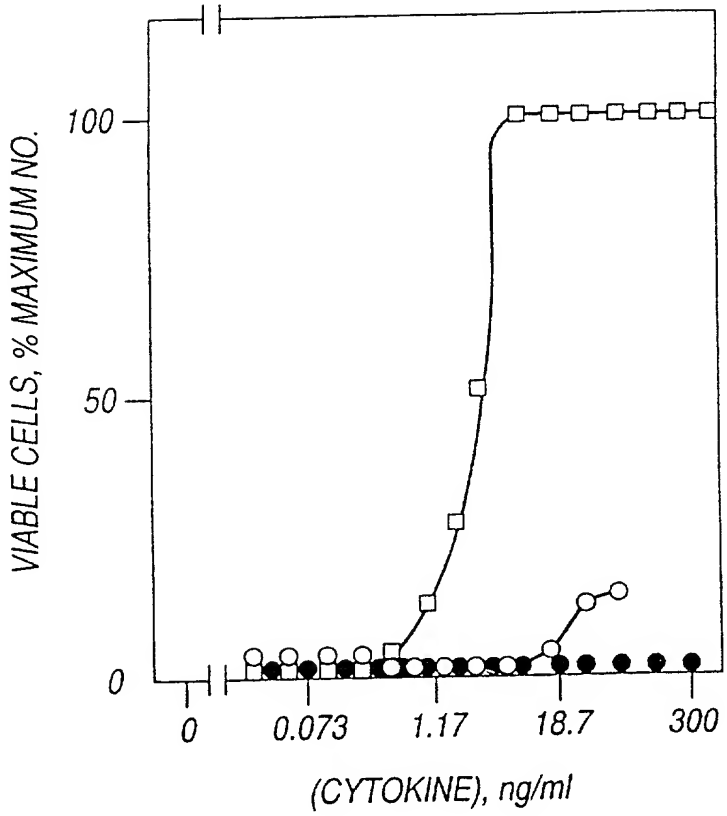
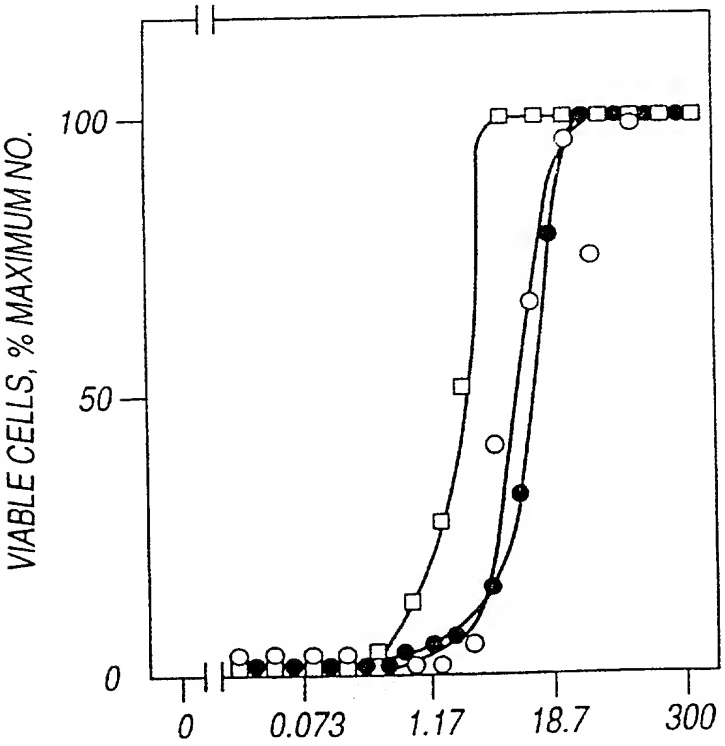

100
50
0
VIABLE CELLS, % MAXIMUM NO.
0
0.073
1.17
18.7
300
(CYTOKINE), ng/ml

Fig. 5(A)


100
50
0
VIABLE CELLS, % MAXIMUM NO.
0
0.073
1.17
18.7
300

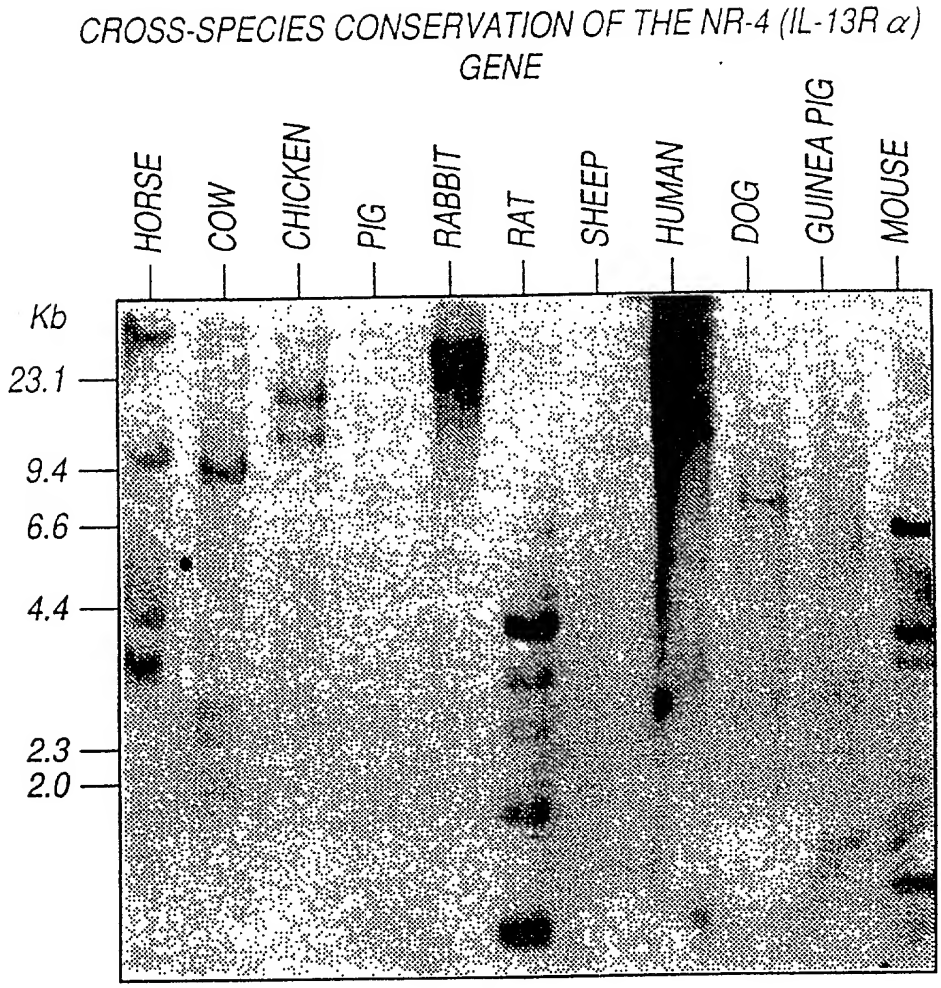


Fig. 6

(major)

DYKDD DDYKD DDESR TEVQP PVTXL SV
1 5 10 15 20 25

(minor)

ASISS SDYKD DDESR TEVQP PVTXL SV
1 5 10 15 20 25

14/24	15/24
16/24	17/24
18/24	19/24
20/24	21/24
22/24	23/24

Fig. 7

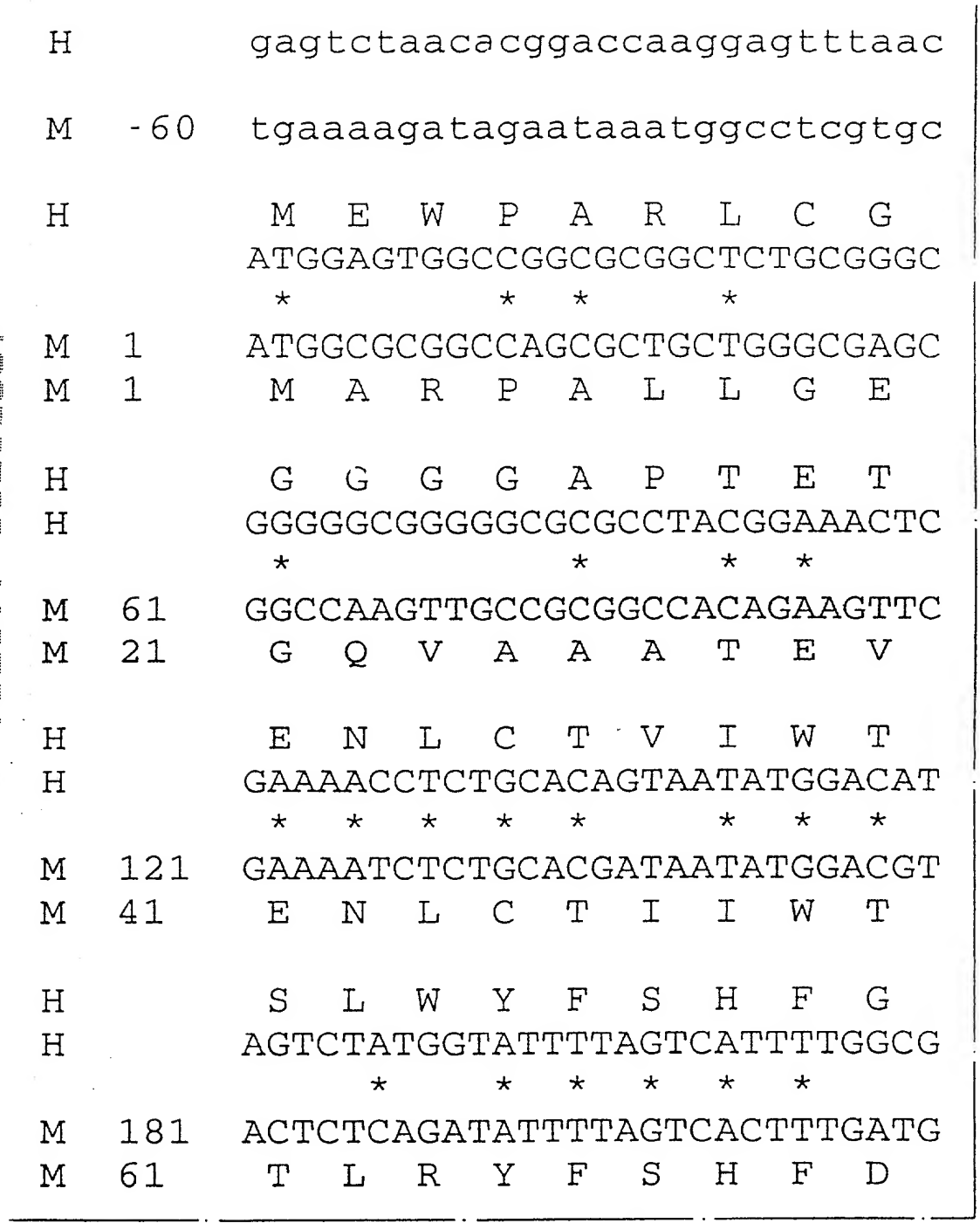

H gagtctaacacggaccaaggagtttaac
M -60 tgaaaagatagaataaatggcctcgtgc
H M E W P A R L C G
ATGGAGTGGCCGGCGCGGCTCTGCGGGC
M 1 ATGGCGCGGCCAGCGCTGCTGGGCGAGC
M 1 M A R P A L L G E
H G G G G A P T E T
H GGGGGCGGGGGCGCGCCTACGGAAACTC
M 61 GGCCAAGTTGCCGCGGCCACAGAAGTTC
M 21 G Q V A A A T E V
H E N L C T V I W T
H GAAAACCTCTGCACAGTAATATGGACAT
M 121 GAAAATCTCTGCACGATAATATGGACGT
M 41 E N L C T I I W T
H S L W Y F S H F G
H AGTCTATGGTATTTTAGTCATTTTGGCG
M 181 ACTCTCAGATATTTTAGTCACTTTGATG
M 61 T L R Y F S H F D

Fig. 7(i)

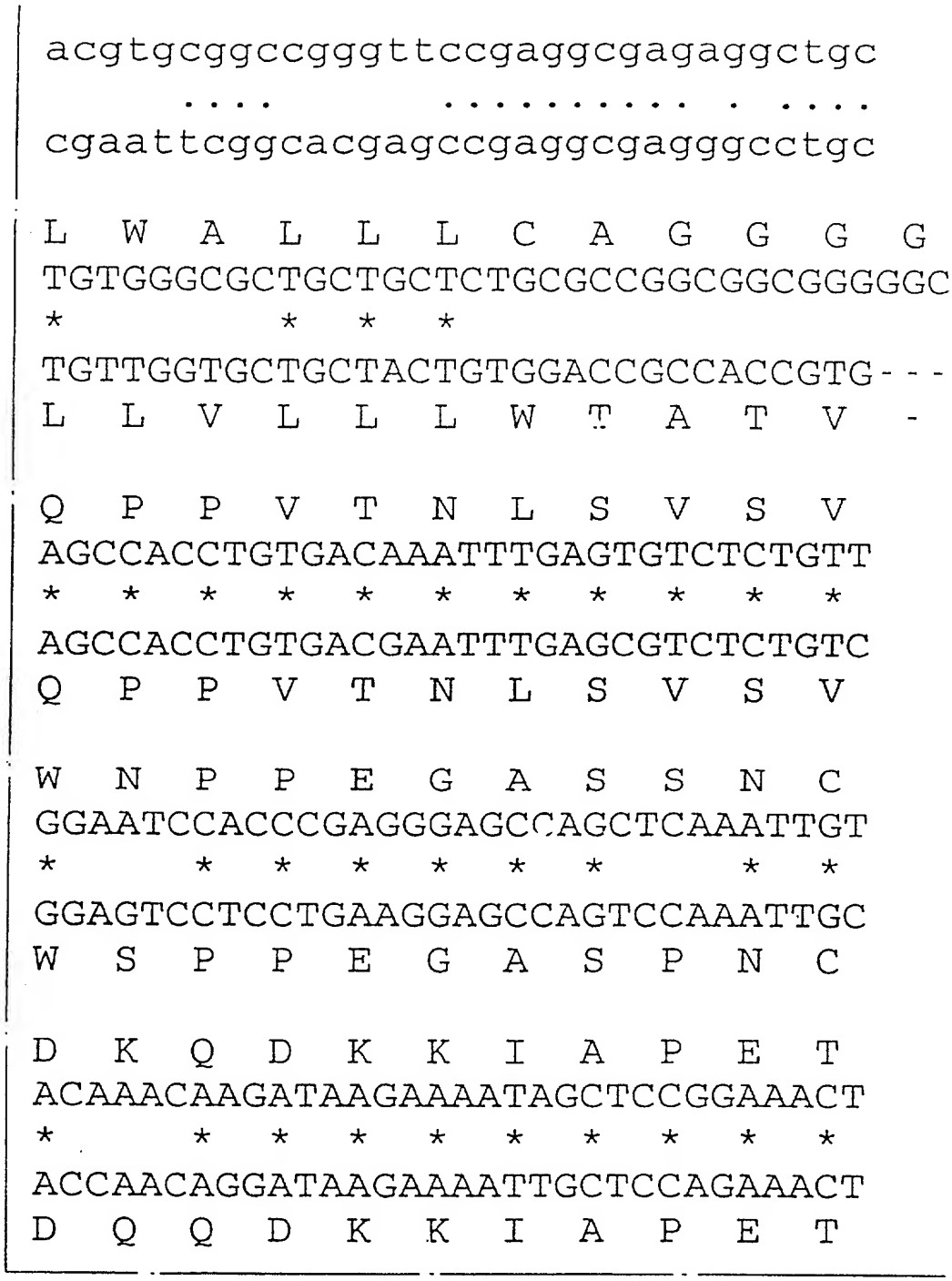

acgtgcggccgggttccgaggcgagaggctgc
cgaattcggcacgagccgaggcgagggcctgc
L W A L L L C A G G G G
TGTGGGCGCTGCTGCTCTGCGCCGGCGGCGGGGGC
TGTTGGTGCTGCTACTGTGGACCGCCACCGTG---
L L V L L L W T A T V -
Q P P V T N L S V S V
AGCCACCTGTGACAAATTTGAGTGTCTCTGTT
AGCCACCTGTGACGAATTTGAGCGTCTCTGTC
Q P P V T N L S V S V
W N P P E G A S S N C
GGAATCCACCCGAGGGAGCCAGCTCAAATTGT
GGAGTCCTCCTGAAGGAGCCAGTCCAAATTGC
W S P P E G A S P N C
D K Q D K K I A P E T
ACAAACAAGATAAGAAAATAGCTCCGGAAACT
ACCAACAGGATAAGAAAATTGCTCCAGAAACT
D Q Q D K K I A P E T

Fig. 7(ii)

```
H          R  R  S  I  E  V  P  L  N
H         CGTCGTTCAATAGAAGTACCCCTGAATG
               *        *     *  *
M  241    CATCGTAAAGAGGAATTACCCCTGGATG
M  81       H  R  K  E  E  L  P  L  D

H          S  T  N  E  S  E  K  P  S
H         AGCACCAATGAGAGTGAGAAGCCTAGCA
           *     *  *  *  *  *  *  *
M  301    AGTGCCAATGAAAGTGAGAAGCCTAGCC
M  101     S  A  N  E  S  E  K  P  S

H          G  D  P  E  S  A  V  T  E
H         GGTGATCCTGAGTCTGCTGTGACTGAAC
           *  *  *  *  *  *  *  *  *
M  361    GGTGATCCTGAGTCCGCTGTGACTGAGC
M  121     G  D  P  E  S  A  V  T  E

H          K  C  S  W  L  P  G  R  N
H         AAGTGTTCTTGGCTCCCTGGAAGGAATA
           *  *  *  *  *  *  *  *  *
M  421    AAGTGTTCCTGGCTCCCTGGAAGGAATA
M  141     K  C  S  W  L  P  G  R  N

H          W  H  R  S  L  E  K  I  H
H         TGGCACAGAAGCCTGGAAAAAATTCATC
```

Fig. 7(iii)

```
E  R  I  C  L  Q  V  G  S  Q  C
AGAGGATTTGTCTGCAAGTGGGGTCCCAGTGT
*     *  *  *  *  *  *  *  *  *
AGAAAATCTGTCTGCAGGTGGGCTCTCAGTGT
E  K  I  C  L  Q  V  G  S  Q  C

I  L  V  E  K  C  I  S  P  P  E
TTTTGGTTGAAAAATGCATCTCACCCCCAGAA
   *  *  *  *  *  *  *  *  *  *
CTTTGGTGAAAAAGTGCATCTCACCCCCTGAA
P  L  V  K  K  C  I  S  P  P  E

L  Q  C  I  W  H  N  L  S  Y  M
TTCAATGCATTTGGCACAACCTGAGCTACATG
*     *  *  *  *  *  *  *  *  *
TCAAGTGCATTTGGCATAACCTGAGCTATATG
L  K  C  I  W  H  N  L  S  Y  M

T  S  P  D  T  N  Y  T  L  Y  Y
CCAGTCCCGACACTAACTATACTCTCTACTAT
*  *  *  *  *     *  *  *  *  *
CAAGCCCTGACACACACTATACTCTGTACTAT
T  S  P  D  T  H  Y  T  L  Y  Y

Q  C  E  N  I  F  R  E  G  Q  Y
AATGTGAAAACATCTTTAGAGAAGGCCAATAC
```

Fig. 7(iv)

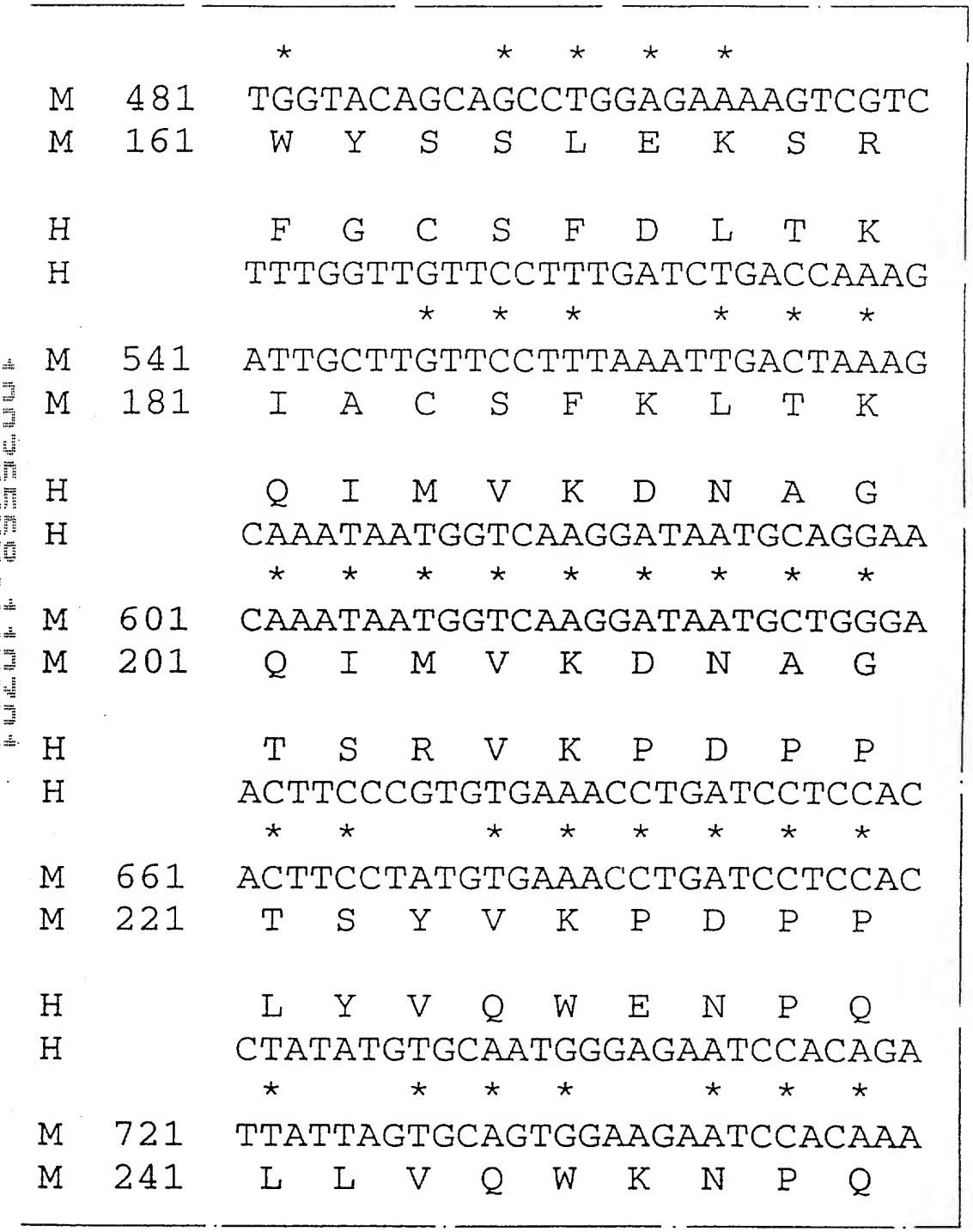

* * * * *
M 481 TGGTACAGCAGCCTGGAGAAAAGTCGTC
M 161 W Y S S L E K S R
H F G C S F D L T K
H TTTGGTTGTTCCTTTGATCTGACCAAAG
* * * * * *
M 541 ATTGCTTGTTCCTTTAAATTGACTAAAG
M 181 I A C S F K L T K
H Q I M V K D N A G
H CAAATAATGGTCAAGGATAATGCAGGAA
* * * * * * * * *
M 601 CAAATAATGGTCAAGGATAATGCTGGGA
M 201 Q I M V K D N A G
H T S R V K P D P P
H ACTTCCCGTGTGAAACCTGATCCTCCAC
* * * * * * * *
M 661 ACTTCCTATGTGAAACCTGATCCTCCAC
M 221 T S Y V K P D P P
H L Y V Q W E N P Q
H CTATATGTGCAATGGGAGAATCCACAGA
* * * * * * *
M 721 TTATTAGTGCAGTGGAAGAATCCACAAA
M 241 L L V Q W K N P Q

Fig. 7(v)

```
 *   *   *   *   *       *   *   *   *
AATGTGAAAACATCTATAGAGAAGGTCAACAC
Q   C   E   N   I   Y   R   E   G   Q   H

V   K   D   S   S   F   E   Q   H   S   V
TGAAGGATTCCAGTTTTGAACAACACAGTGTC
*               *   *   *               *
TGGAACCT---AGTTTTGAACATCAGAACG TT
V   E   P   -   S   F   E   H   Q   N   V

K   I   K   P   S   F   N   I   V   P   L
AAATTAAACCATCCTTCAATATAGTGCCTTTA
*   *       *   *           *   *       *
AAATTAGGCCATCCTGCAAAATAGTGTCTTTA
K   I   R   P   S   C   K   I   V   S   L

H   I   K   N   L   S   F   H   N   D   D
ATATTAAAAACCTCTCCTTCCACAATGATGAC
*   *   *       *               *
ATATTAAACATCTTCTCCTCAAAAATGGTGCC
H   I   K   H   L   L   L   K   N   G   A

N   F   I   S   R   C   L   F   Y   E   V
ATTTTATTAGCAGATGCCTATTTTATGAAGTA
*   *       *   *   *   *       *   *   *
ATTTTAGAAGCAGATGCTTAACTTATGAAGTG
N   F   R   S   R   C   L   T   Y   E   V
```

Fig. 7(vi)

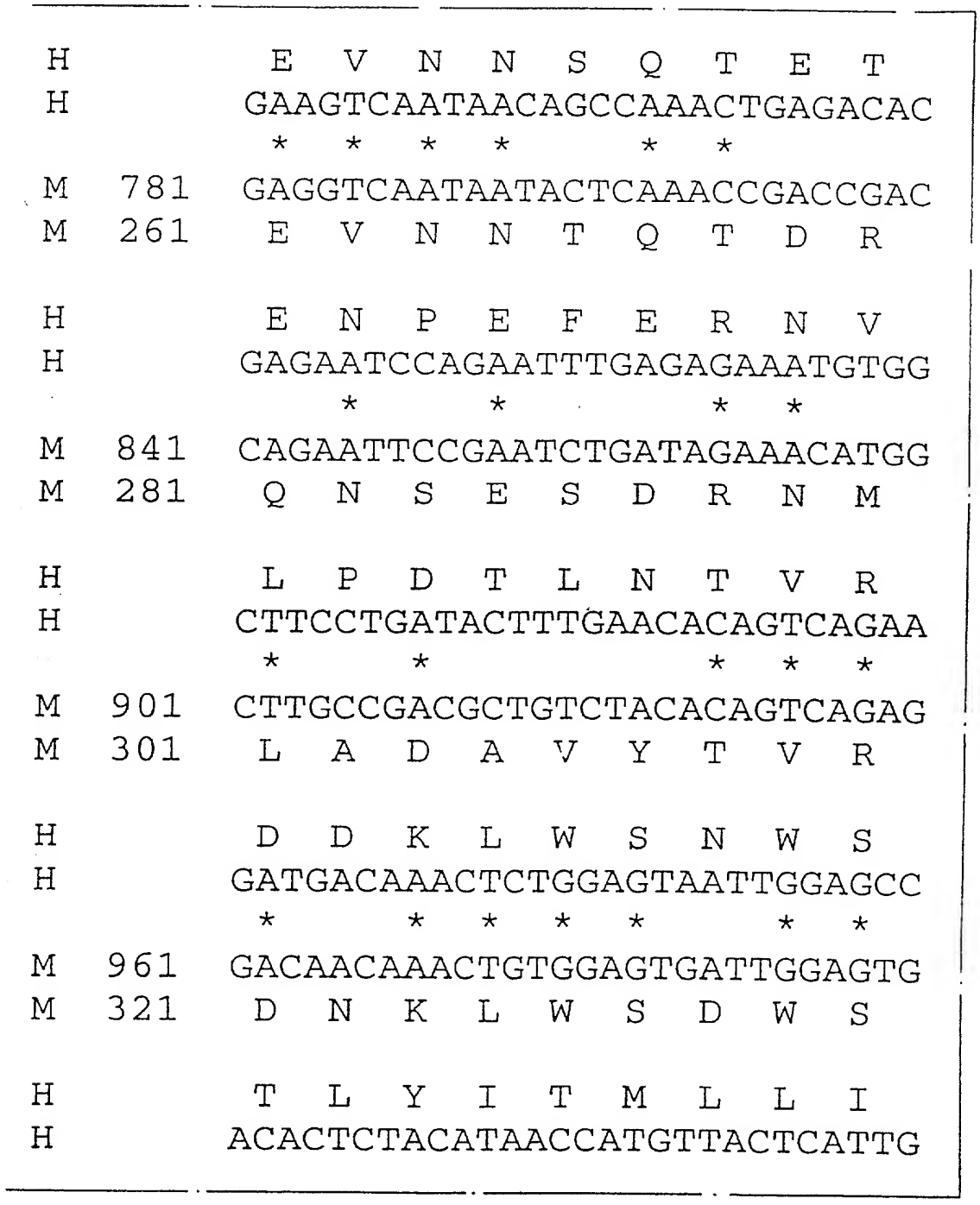

H E V N N S Q T E T
H GAAGTCAATAACAGCCAAACTGAGACAC
* * * * * *
M 781 GAGGTCAATAATACTCAAACCGACCGAC
M 261 E V N N T Q T D R
H E N P E F E R N V
H GAGAATCCAGAATTTGAGAGAAATGTGG
* * * *
M 841 CAGAATTCCGAATCTGATAGAAACATGG
M 281 Q N S E S D R N M
H L P D T L N T V R
H CTTCCTGATACTTTGAACACAGTCAGAA
* * * * *
M 901 CTTGCCGACGCTGTCTACACAGTCAGAG
M 301 L A D A V Y T V R
H D D K L W S N W S
H GATGACAAACTCTGGAGTAATTGGAGCC
* * * * * * *
M 961 GACAACAAACTGTGGAGTGATTGGAGTG
M 321 D N K L W S D W S
H T L Y I T M L L I
H ACACTCTACATAACCATGTTACTCATTG

Fig. 7(vii)

```
H   N   V   F   Y   V   Q   E   A   K   C
ATAATGTTTTCTACGTCCAAGAGGCTAAATGT
*   *               *       *       *   *
ATAATATTTTAGAGGTTGAAGAGGACAAATGC
H   N   I   L   E   V   E   E   D   K   C

E   N   T   S   C   F   M   V   P   G   V
AGAATACATCTTGTTTCATGGTCCCTGGTGTT
*       *   *   *   *           *   *   *
AGGGTACAAGTTGTTTCCAACTCCCTGGTGTT
E   G   T   S   C   F   Q   L   P   G   V

I   R   V   K   T   N   K   L   C   Y   E
TAAGAGTCAAAACAAATAAGTTATGCTATGAG
    *   *   *   *   *   *   *   *
TAAGAGTCAAAACAAACAAGTTATGCTTTGAT
V   R   V   K   T   N   K   L   C   F   D

Q   E   M   S   I   G   K   K   R   N   S
AAGAAATGAGTATAGGTAAGAAGCGCAATTCC
            *   *   *   *           *   *
AAGCACAGAGTATAGGTAAGGAGCAAAACTCC
E   A   Q   S   I   G   K   E   Q   N   S

V   P   V   I   V   A   G   A   I   I   V
TTCCAGTCATCGTCGCAGGTGCAATCATAGTA
```

Fig. 7(viii)

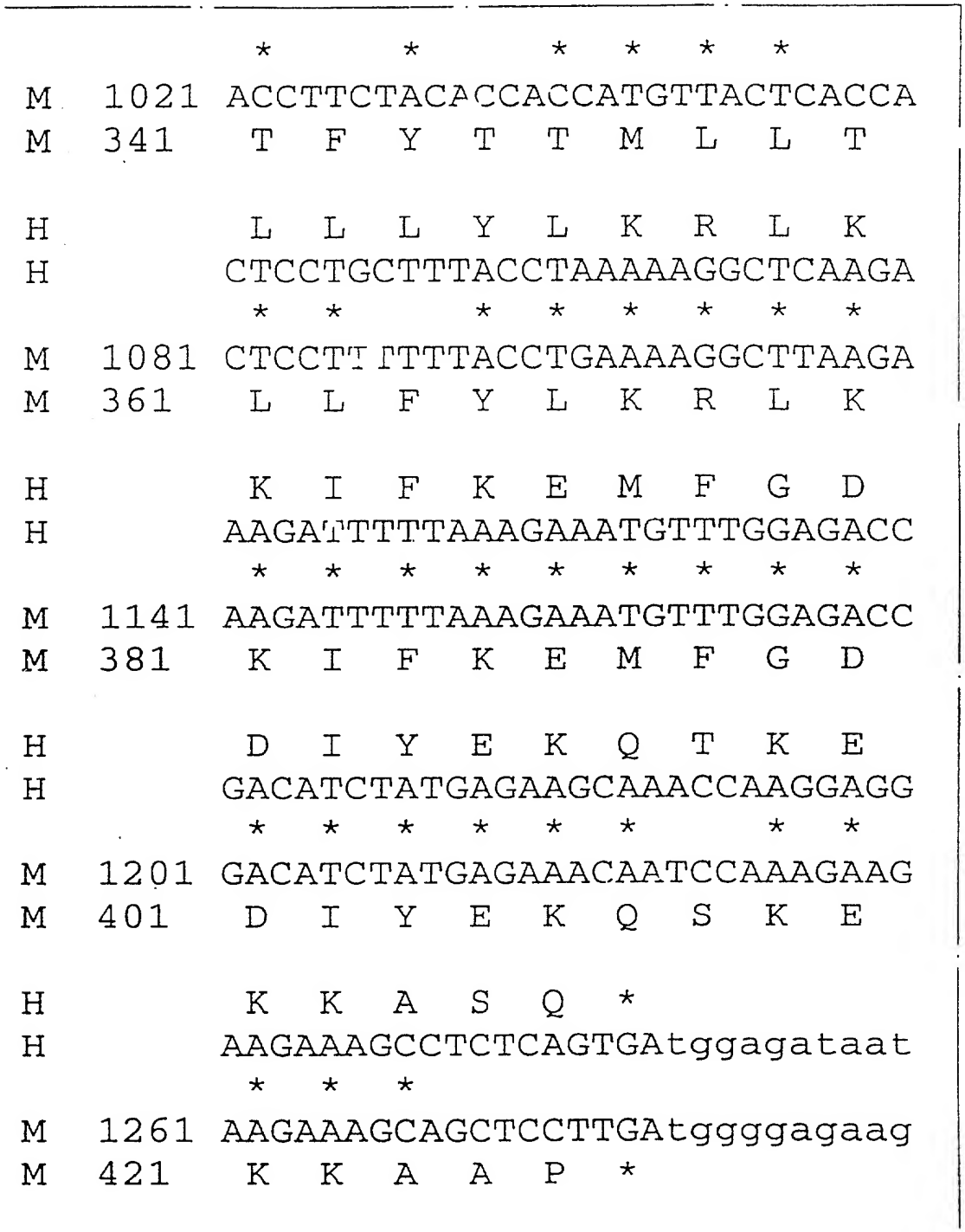

* * * * * *
M 1021 ACCTTCTACACCACCATGTTACTCACCA
M 341 T F Y T T M L L T
H L L L Y L K R L K
H CTCCTGCTTTACCTAAAAAGGCTCAAGA
* * * * * * * *
M 1081 CTCCTTTTTTACCTGAAAAGGCTTAAGA
M 361 L L F Y L K R L K
H K I F K E M F G D
H AAGATTTTTAAAGAAATGTTTGGAGACC
* * * * * * * * *
M 1141 AAGATTTTTAAAGAAATGTTTGGAGACC
M 381 K I F K E M F G D
H D I Y E K Q T K E
H GACATCTATGAGAAGCAAACCAAGGAGG
* * * * * * * *
M 1201 GACATCTATGAGAAACAATCCAAAGAAG
M 401 D I Y E K Q S K E
H K K A S Q *
H AAGAAAGCCTCTCAGTGAtggagataat
* * *
M 1261 AAGAAAGCAGCTCCTTGAtggggagaag
M 421 K K A A P *

Fig. 7(ix)

```
    *   *       *   *       *       *
TTCCAGTCTTTGTCGCAGTGGCAGTCATAATC
I   P   V   F   V   A   V   A   V   I   I

I   I   I   F   P   P   I   P   D   P   G
TTATTATATTCCCTCCAATTCCTGATCCTGGC
*   *   *   *   *   *   *   *   *   *   *
TCATTATATTTCCTCCAATTCCTGATCCTGGC
I   I   I   F   P   P   I   P   D   P   G

Q   N   D   D   T   L   H   W   K   K   Y
AGAATGATGATACTCTGCACTGGAAGAAGTAC
*   *   *   *   *   *   *   *   *   *   *
AGAATGATGATACCCTGCACTGGAAGAAGTAT
Q   N   D   D   T   L   H   W   K   K   Y

E   T   D   S   V   V   L   I   E   N   L
AAACCGACTCTGTAGTGCTGATAGAAAACCTG
*   *   *   *   *   *   *   *   *   *   *
AAACGGATTCTGTAGTGCTGATAGAAAACCTG
E   T   D   S   V   V   L   I   E   N   L


ttatttttaccttcactgtgaccttgagaaga

tgatttctttcttgccttcaatgtgaccctgt
```

Fig. 7(x)

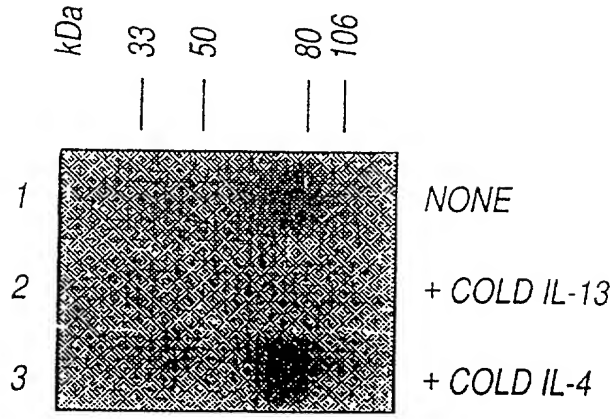

kDa
33
50
80
106
1
2
3
NONE
+ COLD IL-13
+ COLD IL-4

Fig. 8

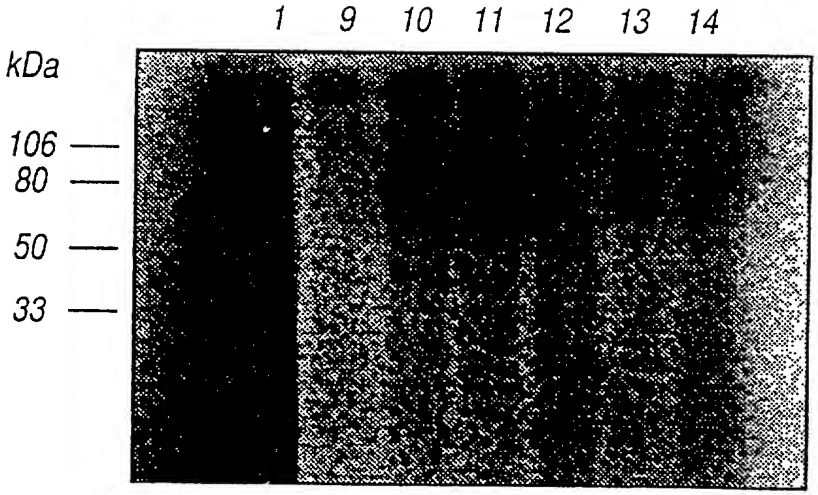

1
9
10
11
12
13
14
kDa
106
80
50
33

Fig. 9